In the Specification:

Please replace paragraph 1 at page 16 of the specification with the following paragraph:

Next, the DNA fragment was isolated from the position at which the blue band appeared, and used to prepare a DNA library as in the third step. The DNA library was subjected repetitively to Southern blotting to select a plasmid carrying the *PRC1* gene, called plasmid pKH4.5. The plasmid pKH4.5 was deposited in the Korean Collection for Type Culture (KCTC), placed in Korea Research Institute of Bioscience and Biotechnology(KRIBB), #52, Oun-dong, Yusong-ku, Taejon 305-333, Republic of Korea, on the date of Feb. 18, 2000 and it was accepted under the accession number of KCTC 0731BP. Double digestion with restriction enzymes *Eco*RI/*Hin*dIII reduced the DNA fragment from about 4.5 kb to about 3.9 kb. The plasmid harboring the *Eco*RI/*Hin*dIII DNA fragment, was called pKH3.9. The restriction site mapping and base sequencing of the *Hansenula polymorpha* DL1 *PRC1* gene was conducted as illustrated in Fig. 3. The base sequence of the [[*PRC1*]] KEX1 gene is given in [[Sequence 3]] SEQ ID NO:3. This DNA sequence was registered as AF090325 with GenBank on Sep. 4, 1998. Analysis of the base sequence revealed that the *Hansenula polymorpha* DL1 *KEX1* gene is 1,833 bp long with no introns. When being deduced from [[Sequence 2]] SEQ ID NO:3, the amino acid sequence of the *Hansenula polymorpha* DL1 *KEX1* gene exhibits as low as 20% homology to the carboxypeptidase α of *Sacchromyces cerevisiae*. However, in the 176th amino acid reside, which is identified to be a serine acting as a catalytic group within an active site of serine protease, there is found high homology to carboxypeptidase α as well as carboxypeptidase Y. Amino acid analysis according to Von Heijne s method (Von Heijne, *J. Mol. Biol.*, 173: 243 (1984)) divulged the presence of a signal peptide consisting of 18 amino acid residues.